



(1) GENERAL INFORMATION:

(i) APPLICANT: Susan DYMECKI

(ii) TITLE OF INVENTION: Use of Flp Recombinase in Mice

(iii) NUMBER OF SEQUENCES: 23

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.

(B) STREET: 1100 New York Avenue, N.W.

(C) CITY: Washington

(D) STATE: D.C.

(E) COUNTRY: USA

(F) ZIP: 20005-3918

G1  
(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: Microsoft Word

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/866,279

(B) FILING DATE: 30-MAY-1997

(C) CLASSIFICATION:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGGTGAAGT TCCTATTCCG AAGTTCCAT TCTCTAGAAA GTATAGGAAC	50
TTCCCTAGGA GATCTTCGAA GGCTCGAGC	79

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TAGCTACGTA GAAGTTCCCTA TTCCGAAGTT CCTATTCTCT AGAAAGTATA	50
GGAACCTTCA	59

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTAGGGAAAGT TCCTATACCTT TCTAGAGAAT AGGAACCTCG GAATAGGAAC	50
TTCA	54

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCGGTGAAGT TCCTATACCTT TCTAGAGAAT AGGAACCTCG GAATAGGAAC	50
TTCTACGTAG CTAGCTCGAG CCTTCGAAGA TCTC	84

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTAAGGTACC GGTGAAGTTC CTA

23

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTCACCCACC GGTGAAGTTC CTA

23

51

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 211 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGTACCGAGC TCAGGCCACCA TGACTGCTCC AAAGAAGAAG CGTAAGGTAC  
CGGTGAAGTT CCTATTCCGA AGTTCTTATT CTCTAGAAAG TATAGGAACCT  
TCACCGGTGG GTGAAGACCA GAAACAGCAC CTCGAACCTGA GCCGCGATAT  
TGCCCAGCGT TTCAACGCGC TGTATGGCGA GATCGATCCC GTCGTTTAC  
AACGTCGTGA C

50

100

150

200

211

~

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Thr Ala Pro Lys Lys Lys Arg Lys Val Pro Val Lys Phe Leu  
1 5 10 15

Phe Arg Ser Ser Tyr Ser Leu Glu Ser Ile Gly Thr Ser Pro Val  
20 25 30

Gly Glu Asp Gln Lys Gln His Leu Glu Leu Ser Arg Asp Ile Ala  
35 40 45

Gln Arg Phe Asn Ala Leu Tyr Gly Glu Ile Asp Pro Val Val Leu  
50 55 60

Gln Arg Arg Asp

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala Pro Lys Lys Lys Arg Lys Val  
1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys Phe Leu Phe Arg Ser Ser Tyr Ser Leu Glu Ser Ile Gly Thr  
1 5 10 15

Ser

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Pro Val Gly Glu Asp Gln Lys Gln His Leu Glu Leu Ser Arg Asp  
1                   5                   10                   15  
Ile Ala Gln Arg Phe Asn Ala Leu Tyr Gly Glu Ile  
20                   25

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAAGTTCCCTA TTC   13

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAAGTTCCCTA TAC   13

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAAAGTTCCTA TTCTCTAGAA AGTATAGGAA CTTC

34

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 48 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAAAGTTCCTA TTCCGAAGTT CCTATTCTCT AGAAAGTATA GGAACCTC

48

(2) INFORMATION FOR SEQ ID NO:16:

G1  
 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGCCACAAT TTGATATATT ATGTAAAACA CCACCTAAGG TGCTTGTTCG TCAGTTGTG	60
GAAAGGTTTG AAAGACCTTC AGGTGAGAAA ATAGCATTAT GTGCTGCTGA ACTAACCTAT	120
TTATGTTGGA TGATTACACA TAACGGAACA GCAATCAAGA GAGCCACATT CATGAGCTAT	180
AATACTATCA TAAGCAATTC GCTGAGTTG GATATTGTCA ACAAGTCACT GCAGTTAAA	240
TACAAGACGC AAAAGCAAC AATTCTGGAA GCCTCATCAA AGAAATTGAT TCCTGCTTGG	300
GAATTACAA TTATTCCTTA CTATGGACAA AAACATCAAT CTGATATCAC TGATATTGTA	360
AGTAGTTGC AATTACAGTT CGAACATCG GAAGAAGCAG ATAAGGGAAA TAGCCACAGT	420
AAAAAAATGC TTAAAGCACT TCTAAGTGAG GGTGAAAGCA TCTGGGAGAT CACTGAGAAA	480
ATACTAAATT CGTTGAGTA TACTCGAGA TTTACAAAAA CAAAAACTTT ATACCAATT	540
CTCTTCCTAG CTACTTCAT CAATTGTGGA AGATTCAGCG ATATTAAGAA CGTTGATCCG	600

AAATCATTAA ATTAGTCCA AAATAAGTAT CTGGGAGTAA TAATCCAGTG TTTAGTGACA 660  
 GAGACAAAGA CAAGCGTTAG TAGGCACATA TACTTCTTTA GCGCAAGGGG TAGGATCGAT 720  
 CCACTTGTAT ATTTGGATGA ATTTTGAGG AATTCTGAAC CAGTCCTAAA ACGAGTAAAT 780  
 AGGACCGGCA ATTCTTCAAG CAACAAGCAG GAATACCAAT TATTAAGA TAACTTAGTC 840  
 AGATCGTACA ACAAAAGCTT GAAGAAAAAT GCGCCTTATT CAATCTTGC TATAAAAAAT 900  
 GGCCCCAAAT CTCACATTGG AAGACATTG ATGACCTCAT TTCTTCAAT GAAGGGCCTA 960  
 ACGGAGTTGA CTAATGTTGT GGGAAATTGG AGCGATAAGC GTGCTTCTGC CGTGGCCAGG 1020  
 ACAACGTATA CTCATCAGAT AACAGCAATA CCTGATCACT ACTTCGCACT AGTTTCTCGG 1080  
 TACTATGCAT ATGATCCAAT ATCAAAGGAA ATGATAGCAT TGAGGATGA GACTAATCCA 1140  
 ATTGAGGAGT GGCAGCATAT AGAACAGCTA AAGGGTAGTG CTGAAGGAAG CATAcgatAC 1200  
 CCCGCATGGA ATGGGATAAT ATCACAGGAG GTACTAGACT ACCTTTCATC CTACATAAAAT 1260  
 AGACGCATAT AA 1272

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu	
1 5 10 15	
Val Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys	
20 25 30	
Ile Ala Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile	
35 40 45	
Thr His Asn Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr	
50 55 60	
Asn Thr Ile Ile Ser Asn Ser Leu Ser Leu Asp Ile Val Asn Lys	
65 70 75	
Ser Leu Gln Phe Lys Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu	
80 85 90	
Ala Ser Leu Lys Lys Leu Ile Pro Ala Trp Glu Phe Thr Ile Ile	
95 100 105	
Pro Tyr Tyr Gly Gln Lys His Gln Ser Asp Ile Thr Asp Ile Val	
110 115 120	

Ser Ser Leu Gln Leu Gln Phe Glu Ser Ser Glu Glu Ala Asp Lys  
                   125                         130                  135  
 Gly Asn Ser His Ser Lys Lys Met Leu Lys Ala Leu Leu Ser Glu  
                   140                         145                  150  
 Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys Ile Leu Asn Ser Phe  
                   155                         160                  165  
 Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr Leu Tyr Gln Phe  
                   170                         175                  180  
 Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe Ser Asp Ile  
                   185                         190                  195  
 Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn Lys Tyr  
                   200                         205                  210  
 Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr Ser  
                   215                         220                  225  
 Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp  
                   230                         235                  240  
 Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val  
                   245                         250                  255  
 Leu Lys Arg Val Asn Arg Thr Gln Asn Ser Ser Ser Asn Lys Gln  
                   260                         265                  270  
 Glu Tyr Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys  
                   275                         280                  285  
 Ala Leu Lys Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn  
                   290                         295                  300  
 Gly Pro Lys Ser His Ile Gly Arg His Leu Met Thr Ser Phe Leu  
                   305                         310                  315  
 Ser Met Lys Gly Leu Thr Glu Leu Thr Asn Val Val Gly Asn Trp  
                   320                         325                  330  
 Ser Asp Lys Arg Ala Ser Ala Val Ala Arg Thr Thr Tyr Thr His  
                   335                         340                  345  
 Gln Ile Thr Ala Ile Pro Asp His Tyr Phe Ala Leu Val Ser Arg  
                   350                         355                  360  
 Tyr Tyr Ala Tyr Asp Pro Ile Ser Lys Glu Met Ile Ala Leu Lys  
                   365                         370                  375  
 Asp Glu Thr Asn Pro Ile Glu Glu Trp Gln His Ile Glu Gln Leu  
                   380                         385                  390  
 Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr Pro Ala Trp Asn Gly  
                   395                         400                  405  
 Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser Ser Tyr Ile Asn  
                   410                         415                  420  
 Arg Arg Ile

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATGCCACAAT TTGATATATT ATGTAAAACA CCACCTAAGG TGCTTGTTCG TCAGTTGTG 60  
GAAAGGTTG AAAGACCTTC AGGTGAGAAA ATAGCATTAT GTGCTGCTGA ACTAACCTAT 120  
TTATGTTGGA TGATTACACA TAACGGAACA GCAATCAAGA GAGCCACATT CATGAGCTAT 180  
AATACTATCA TAAGCAATTC GCTGAGTTTC GATATTGTCA ACAAGTCACT GCAGTTAAA 240  
TACAAGACGC AAAAGCAAC AATTCTGGAA GCCTCATTAA AGAAATTGAT TCCTGCTTGG 300  
GAATTTACAA TTATTCTTA CTATGGACAA AAACATCAAT CTGATATCAC TGATATTGTA 360  
AGTAGTTGC AATTACAGTT CGAACATCG GAAGAAGCAG ATAAGGGAAA TAGCCACAGT 420  
AAAAAAATGC TTAAAGCACT TCTAAGTGAG GGTGAAAGCA TCTGGGAGAT CACTGAGAAA 480  
ATACTAAATT CGTTGAGTA TACTCGAGA TTTACAAAAA CAAAAACTTT ATACCAATTC 540  
CTCTTCCTAG CTACTTTCAT CAATTGTGGA AGATTCAAGC ATATTAAGAA CGTTGATCCG 600  
AAATCATTAA AATTAGTCCA AAATAAGTAT CTGGGAGTAA TAATCCAGTG TTTAGTGACA 660  
GAGACAAAGA CAAGCGTTAG TAGGCACATA TACTTCTTA GCGCAAGGGG TAGGATCGAT 720  
CCACTTGTAT ATTTGGATGA ATTTTGAGG AATTCTGAAC CAGTCCTAAA ACGAGTAAAT 780  
AGGACCGGCA ATTCTTCAAG CAACAAGCAG GAATACCAAT TATTAAGA TAACTTAGTC 840  
AGATCGTACA ACAAAAGCTT GAAGAAAAAT GCGCCTTATT CAATCTTGC TATAAAAAAT 900  
GGCCCCAAAT CTCACATTGG AAGACATTG ATGACCTCAT TTCTTCAAT GAAGGGCCTA 960  
ACGGAGTTGA CTAATGTTGT GGGAAATTGG AGCGATAAGC GTGCTTCTGC CGTGGCCAGG 1020  
ACAACGTATA CTCATCAGAT AACAGCAATA CCTGATCACT ACTTCGCACT AGTTCTCGG 1080  
TACTATGCAT ATGATCCAAT ATCAAAGGAA ATGATAGCAT TGAAGGATGA GACTAATCCA 1140  
ATTGAGGAGT GGCAGCATAT AGAACAGCTA AAGGGTAGTG CTGAAGGAAG CATACTGATAC 1200  
CCCGCATGGA ATGGGATAAT ATCACAGGAG GTACTAGACT ACCTTCATC CTACATAAAAT 1260  
AGACGCATAT AA 1272

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu  
1 5 10 15

Val Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys  
20 25 30

Ile Ala Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile  
35 40 45

Thr His Asn Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr  
50 55 60

Asn Thr Ile Ile Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys  
65 70 75

Ser Leu Gln Phe Lys Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu  
80 85 90

Ala Ser Leu Lys Lys Leu Ile Pro Ala Trp Glu Phe Thr Ile Ile  
95 100 105

Pro Tyr Tyr Gly Gln Lys His Gln Ser Asp Ile Thr Asp Ile Val  
110 115 120

Ser Ser Leu Gln Leu Gln Phe Glu Ser Ser Glu Glu Ala Asp Lys  
125 130 135

Gly Asn Ser His Ser Lys Lys Met Leu Lys Ala Leu Leu Ser Glu  
140 145 150

Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys Ile Leu Asn Ser Phe  
155 160 165

Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr Leu Tyr Gln Phe  
170 175 180

Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe Ser Asp Ile  
185 190 195

Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn Lys Tyr  
200 205 210

Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr Ser  
215 220 225

Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp  
230 235 240

Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val  
245 250 255

Leu Lys Arg Val Asn Arg Thr Gln Asn Ser Ser Ser Asn Lys Gln  
 260 265 270  
 Glu Tyr Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys  
 275 280 285  
 Ala Leu Lys Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn  
 290 295 300  
 Gly Pro Lys Ser His Ile Gly Arg His Leu Met Thr Ser Phe Leu  
 305 310 315  
 Ser Met Lys Gly Leu Thr Glu Leu Thr Asn Val Val Gly Asn Trp  
 320 325 330  
 Ser Asp Lys Arg Ala Ser Ala Val Ala Arg Thr Thr Tyr Thr His  
 335 340 345  
 Gln Ile Thr Ala Ile Pro Asp His Tyr Phe Ala Leu Val Ser Arg  
 350 355 360  
 Tyr Tyr Ala Tyr Asp Pro Ile Ser Lys Glu Met Ile Ala Leu Lys  
 365 370 375  
 Asp Glu Thr Asn Pro Ile Glu Glu Trp Gln His Ile Glu Gln Leu  
 380 385 390  
 Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr Pro Ala Trp Asn Gly  
 395 400 405  
 Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser Ser Tyr Ile Asn  
 410 415 420

G / Arg Arg Ile

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGTCCAACTG CAGCCCAAGC TTCC

24

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:  
GTGGATCGAT CCTACCCCTT GCG

23

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GACTGCTCCA AAGAAGAAGC GTAAGG

26

9 / (2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCTATTACGC CAGCTGGCGA AAGG

24